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OM protein - protein search, using sw model

Run on: March 1, 2006, 22:37:13 ; Search time 164 Seconds

(without alignments)
723.558 Million cell updates/sec

Title: US-09-245-198A-4

Perfect score: 1444

Sequence: 1 MSLLDFEISARRLPRLPRSLG.....PWAHLKAPFLTYFGLPQVH 284

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_Main:*

1: /cgn2_6/prodata/1/pubpaas/us07_pubcomb.pep:*

2: /cgn2_6/prodata/1/pubpaas/us08_pubcomb.pep:*

3: /cgn2_6/prodata/1/pubpaas/us09_pubcomb.pep:*

4: /cgn2_6/prodata/1/pubpaas/us10_pubcomb.pep:*

5: /cgn2_6/prodata/1/pubpaas/us10s_pubcomb.pep:*

6: /cgn2_6/prodata/1/pubpaas/us11_pubcomb.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1444	100.0	284	5 US-10-978-203-4	Sequence 4, Appli
2	1444	100.0	284	5 US-10-978-311-4	Sequence 4, Appli
3	1268	87.8	249	3 US-09-905-810-2	Sequence 2, Appli
4	1268	87.8	249	3 US-09-782-910-44	Sequence 44, Appli
5	1268	87.8	249	4 US-10-218-947-24	Sequence 24, Appli
6	1268	87.8	249	4 US-10-211-951-4	Sequence 4, Appli
7	1268	87.8	249	4 US-10-211-984-4	Sequence 4, Appli
8	1268	87.8	249	4 US-10-310-793-30	Sequence 30, Appli
9	1268	87.8	249	4 US-10-211-958-4	Sequence 4, Appli
10	1268	87.8	249	4 US-10-202-062-24	Sequence 24, Appli
11	1268	87.8	249	4 US-10-806-018-44	Sequence 44, Appli
12	1268	87.8	249	5 US-10-825-282-20	Sequence 20, Appli
13	1268	87.8	249	5 US-10-116-141-2	Sequence 2, Appli
14	1066	73.8	249	6 US-11-028-780-24	Sequence 24, Appli
15	1066	73.8	273	3 US-09-742-454A-2	Sequence 2, Appli
16	1066	73.8	273	3 US-09-983-777-2	Sequence 24, Appli
17	1066	73.8	273	5 US-10-754-847-2	Sequence 44, Appli
18	1066	73.8	273	5 US-10-898-575-2	Sequence 2, Appli
19	1066	73.8	273	5 US-10-771-250-2	Sequence 2, Appli
20	1020	70.6	225	3 US-09-905-810-1	Sequence 1, Appli
21	1020	70.6	225	5 US-10-911-141-1	Sequence 1, Appli
22	1020	70.6	225	5 US-10-978-203-12	Sequence 2, Appli
23	1020	70.6	225	5 US-10-978-131-2	Sequence 2, Appli
24	731	50.6	141	5 US-10-778-890-11	Sequence 11, Appli
25	504	34.9	98	4 US-10-338-063-14	Sequence 14, Appli
26	504	34.9	98	4 US-10-311-399-14	Sequence 14, Appli
27	504	34.9	98	5 US-10-794-751-14	Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-10-978-203-4
; Sequence 4, Application US/10978203
; Publication No. US20050112666A1
; GENERAL INFORMATION:
; APPLICANT: Chichesterische Yves
; TITLE OF INVENTION: tumor Necrosis Factor Related Ligand
; FILE REFERENCE: A003
; CURRENT APPLICATION NUMBER: US-10/978,203
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/023,541
; PRIOR FILING DATE: 1996-08-07
; PRIOR APPLICATION NUMBER: 60/028,515
; PRIOR FILING DATE: 1996-10-18
; PRIOR APPLICATION NUMBER: 60/040,820
; PRIOR FILING DATE: 1997-03-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSTOQ for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 284
; TYPE: PRT
; ORGANISM: homo sapien
US-10-978-203-4

Query Match 100.0%; Score 1444; DB 5; Length 284;
Best Local Similarity 100.0%; Prod. No. 4_3e-11%;
Matches 284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSLLDFEISARRLPRLPRSLGSRDGGAVRQAQPAPMAARRSQRGRGEPGTALLVPLA 60
1 MSLLDFEISARRLPRLPRSLGSRDGGAVRQAQPAPMAARRSQRGRGEPGTALLVPLA 60
61 LGGLA1AC1GLLIAVQSLGSRASLSAORPAQSLVAYRQDPSLNPOTBESODPAPPL 120
61 LGGLA1AC1GLLIAVQSLGSRASLSAORPAQSLVAYRQDPSLNPOTBESODPAPPL 120
121 NRYQGEFIVTRAGIYLYCQVRFIDEGAVYLQDLYVGVLALRCLEPFSATAASSLGP 180
121 NRYQGEFIVTRAGIYLYCQVRFIDEGAVYLQDLYVGVLALRCLEPFSATAASSLGP 180
121 NRYQGEFIVTRAGIYLYCQVRFIDEGAVYLQDLYVGVLALRCLEPFSATAASSLGP 180
181 YNRQGEFIVTRAGIYLYCQVRFIDEGAVYLQDLYVGVLALRCLEPFSATAASSLGP 240
181 YNRQGEFIVTRAGIYLYCQVRFIDEGAVYLQDLYVGVLALRCLEPFSATAASSLGP 240
241 QRLICQVSSILALRPGSLSRIRLPAWHLKAAPFLTYFGLFQVH 284
241 QRLICQVSSILALRPGSLSRIRLPAWHLKAAPFLTYFGLFQVH 284

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OM protein : protein search, using SW model

Run on: March 1, 2006, 22:37:53 ; Search time 21 Seconds (without alignments)

269.766 Million cell updates/sec

Title: US-09-245-198A-4

Perfect score: 1444

Sequence: 1. MSILDFEISARRLPLRSLG. PWAHLKAAPFLTYFGLFQVH 284

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 133702 seqs, 19947517 residues

Total number of hits satisfying chosen parameters: 133702

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published Applications AA_New:*

1: /cgn2_6/podata/1/pubpaas/US08_NEW_PUB_pep:*

2: /cgn2_6/podata/1/pubpaas/US06_NEW_PUB_pep:*

3: /cgn2_6/podata/1/pubpaas/US07_NEW_PUB_pep:*

4: /cgn2_6/podata/1/pubpaas/US05_NEW_PUB_pep:*

5: /cgn2_6/podata/1/pubpaas/US09_NEW_PUB_pep:*

6: /cgn2_6/podata/1/pubpaas/US10_NEW_PUB_pep:*

7: /cgn2_6/podata/1/pubpaas/US11_NEW_PUB_pep:*

8: /cgn2_6/podata/1/pubpaas/US60_NEW_PUB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	6.9	912	6 US-10-964-313-12	Sequence 12, Appl
2	97	6.7	441	7 US-11-087-099-3892	Sequence 289?, Appl
3	93	6.4	810	6 US-10-954-468-37	Sequence 37, Appl
4	92	6.4	240	6 US-10-987-663-6	Sequence 6, Appl
5	92	6.4	240	7 US-11-136-341A-1	Sequence 1, Appl
6	91.5	6.3	564	7 US-11-124-367A-263	Sequence 263, Appl
7	89.5	6.2	616	6 US-10-858-30-21	Sequence 21, Appl
8	89	6.2	316	7 US-11-032-797-4	Sequence 4, Appl
9	89	6.2	316	7 US-11-238-266-2	Sequence 2, Appl
10	89	6.2	564	7 US-11-087-099-3568	Sequence 356, Appl
11	88.5	6.1	278	6 US-10-861-334-16	Sequence 16, Appl
12	88.5	6.1	278	6 US-10-861-934-26	Sequence 26, Appl
13	88	6.1	281	6 US-10-861-934-8	Sequence 8, Appl
14	88.5	6.1	281	6 US-10-861-334-30	Sequence 30, Appl
15	88.5	6.1	281	7 US-11-213-168-11	Sequence 11, Appl
16	88.5	6.1	281	7 US-11-213-168-12	Sequence 12, Appl
17	88.5	6.1	3073	7 US-11-143-380-50	Sequence 50, Appl
18	87	6.0	291	7 US-11-032-297-6	Sequence 6, Appl
19	87	6.0	427	7 US-11-158-084-350	Sequence 350, Appl
20	86	6.0	241	7 US-11-084-447-5	Sequence 5, Appl
21	84.5	5.9	367	6 US-10-131-826A-208	Sequence 208, Appl
22	84.5	5.9	367	6 US-10-973-115B-208	Sequence 201, Appl
23	84.5	5.9	377	7 US-11-087-099-12099	Sequence 12099, Appl
24	83	5.7	586	7 US-11-072-512-2947	Sequence 2947, Appl
25	82.5	5.7	204	7 US-11-136-341A-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-10-964-313-12

Sequence 12, Application US/10964313
/ Publication No. US20050287629A1
/ GENERAL INFORMATION:
/ APPLICANT: GROZINGER, CHRISTINA M.
/ APPLICANT: HASIG, CHRISTIAN A.
/ APPLICANT: SCHREIBER, STUART L.
/ TITLE OF INVENTION: CLASS II HUMAN HISTONE DEACETYLASES, AND USES RELATED
/ FILM REFERENCE: HUV-037-022
/ CURRENT APPLICATION NUMBER: US/10/964,313
/ CURRENT FILING DATE: 2004-10-13
/ PRIOR APPLICATION NUMBER: 09/800,187
/ PRIOR FILING DATE: 2001-03-05
/ PRIOR APPLICATION NUMBER: 60/1,86,802
/ PRIOR FILING DATE: 2000-03-03
/ NUMBER OF SEQ ID NOS: 73
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 12
/ LENGTH: 912
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-964-313-12

Query Match 6.9%; Score 99; DB 6; Length 912;
Best Local Similarity 24.2%; Pred. No. 0.55; Mismatches 67; Indels 56; Gaps 6;
Matches 46; Conservative 21; Mismatches 67; Indels 56; Gaps 6;

QY 11 RRLPLRSLGSRDGGAVR-----RSORRRGR- 47
Db 361 RQIPLSAEDLTQDGGPGQVVDGGLERHGGPQHQPLQHQPLQHQLWBOORLQLR 420

QY 48 -RGPBPGLTLLVPLAIGLGLACLGLLAVVSGRSASLSAQPAQELVABEDQDPSL 106
Db 421 PRGSTGDTVLLPLAQGGRPLS---RAQSSPAAPASQARVLSSETPART 475

QY 107 NPQT-----BESQDP-----APFLNRLVPRSRAPKGRKTRAR 139
Db 476 LPPPTGLIYDSYMLKHQCSCGDNRSRPEHAGRIQSINSRLQERGLRSOCBLGRKASLS 535

QY 140 RAIAAHYZEV 149
Db 536 BLSQVHSBRH 545

RESULT 2
US-11-087-099-2892

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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 2, 2006, 08:37:41 ; Search time 379 Seconds (without alignments)

1642.836 Million cell updates/sec

Title: US-09-245-198A-4

Perfect score: 1444

Sequence: 1 MSLLDFBISARRLLPRLPRSLG.....PWAHLKAPFLTYFGFLFQVH 284

Scoring table: BLOSUM62

Xgap0 10.0 ; Xgapext 0.5

Ygap0 10.0 ; Ygapext 0.5

Fgap0 6.0 ; Fgapext 7.0

Del0p 6.0 ; Delext 7.0

Searched: 7218512 seqs, 1096188070 residues

Total number of hits satisfying chosen parameters: 14437024

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-NCBIL=frame_p2n.model -DEV=xlh
-Q=abss (ABSSWB) spool/US09245198/runat 01/03/2006 13:50:43 -26897/app_query.fasta_1
-DB=Published Applications/NA_New -QFMT=fastaP -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOC=PUBLIC -LOOPEXT=0 -UNITS=bits -BITS=1 -END=1 -MATRIX=blossom62
-TRANS=human40.cdt -LIST=45 -DOALIGN=200 -THR SCORE=90ct -THR MAX=100
-THR MIN=15 -MODE=LOCAL -OUTEXT=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=20000000 -HOST=abs05 -USER=US09245198 @CGN 1.1 220 @runat 01/03/2006 13:50:43 -26897 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPLBLOCK=100 -LONGLOG -DBV TIMEOUT=120
-WARN TIMEOUT=0 -THREADS=1 -XGAP0P=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

-YGAPOp=10 -YGAPEXT=0.5 -DEL0p=6 -DELEXt=7

Database :

Published_Applications_NA_New.*

1: /cgn2_6/prodata/2/pubna/US08 NEW PUB.seq*

2: /cgn2_6/prodata/2/pubna/US06 NEW PUB.seq*

3: /cgn2_6/prodata/2/pubna/US07 NEW PUB.seq*

4: /cgn2_6/prodata/2/pubna/PCT NEW PUB.seq*

5: /cgn2_6/prodata/2/pubna/US05 NEW PUB.seq*

6: /cgn2_6/prodata/2/pubna/US09 NEW PUB.seq*

7: /cgn2_6/prodata/2/pubna/US10 NEW PUB.seq*

8: /cgn2_6/prodata/2/pubna/US10 NEW PUB.seq*

9: /cgn2_6/prodata/2/pubna/US11 NEW PUB.seq*

10: /cgn2_6/prodata/2/pubna/US11 NEW PUB.seq*

11: /cgn2_6/prodata/2/pubna/US11 NEW PUB.seq*

12: /cgn2_6/prodata/2/pubna/US11 NEW PUB.seq*

13: /cgn2_6/prodata/2/pubna/US60 NEW PUB.seq*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

US-11-136-527-3597

; Sequence 3597, Application US/111365527

; Publication No. US20050287570A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

; FILE REFERENCE: 031896-041000 (AM01086)

; CURRENT APPLICATION NUMBER: US-11-136-527

; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US 60/574,294

; PRIOR FILING DATE: 2005-05-26

; NUMBER OF SEQ ID NOs: 36830

; SOFTWARE: PatentIn Version 3.2

; SEQ ID NO 3597

; LENGTH: 584

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE: misc_feature

; NAME/KEY: misc_feature

; LOCATION: (396)..(396)

; OTHER INFORMATION: n is a, c, g, or t

; FEATURE: misc_feature

; LOCATION: (440)..(440)

; OTHER INFORMATION: n is a, c, g, or t